



FIG. 1

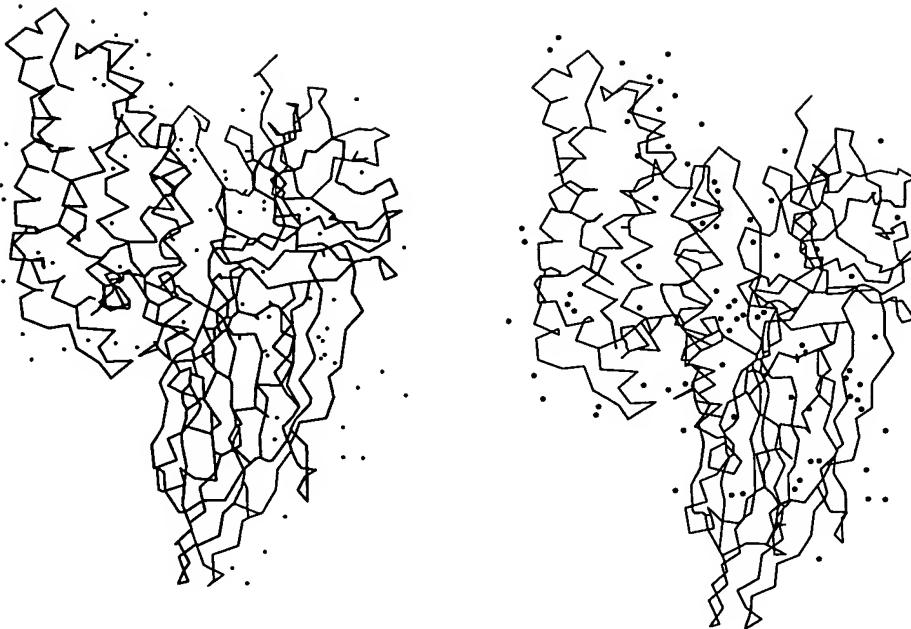


FIG. 2

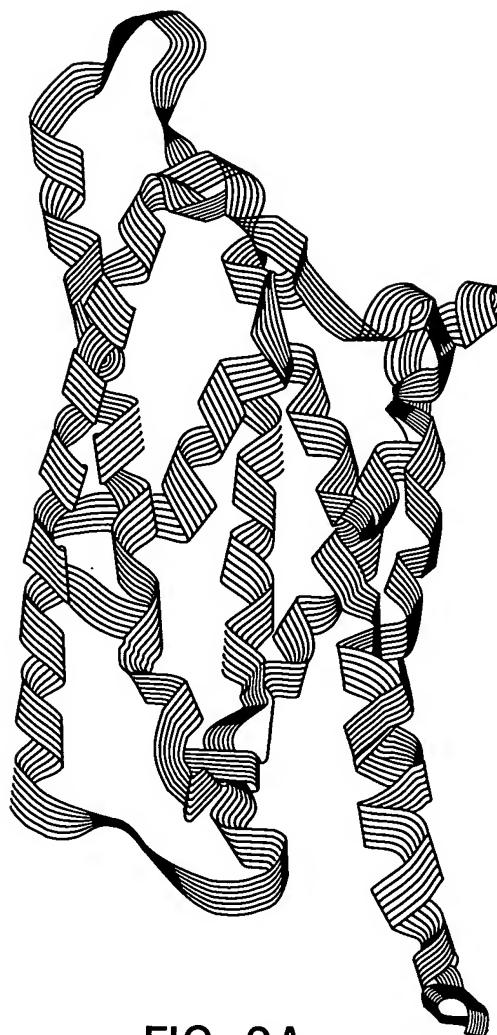


FIG. 3A

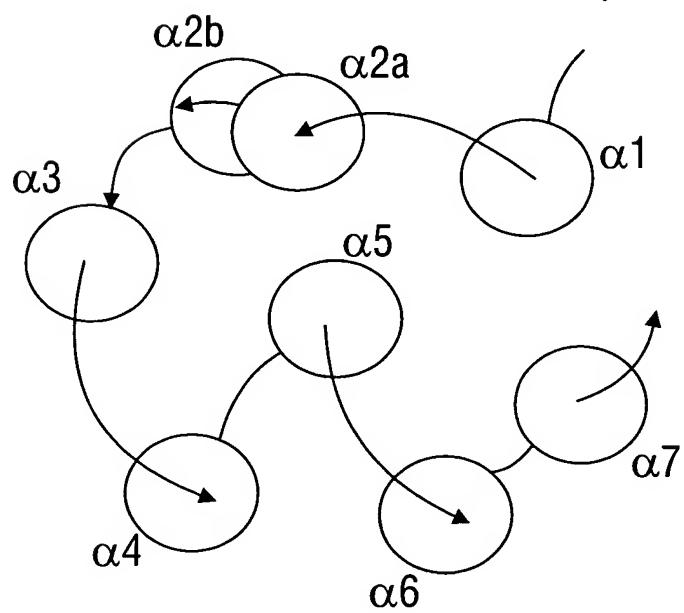


FIG. 3B

alpha helix	Amino acid Residues
α_1	63-79
α_{2a}	85-98
α_{2b}	105-118
α_3	124-153
α_4	161-186
α_5	194-215
α_6	223-255
α_7	260-286

FIG. 4

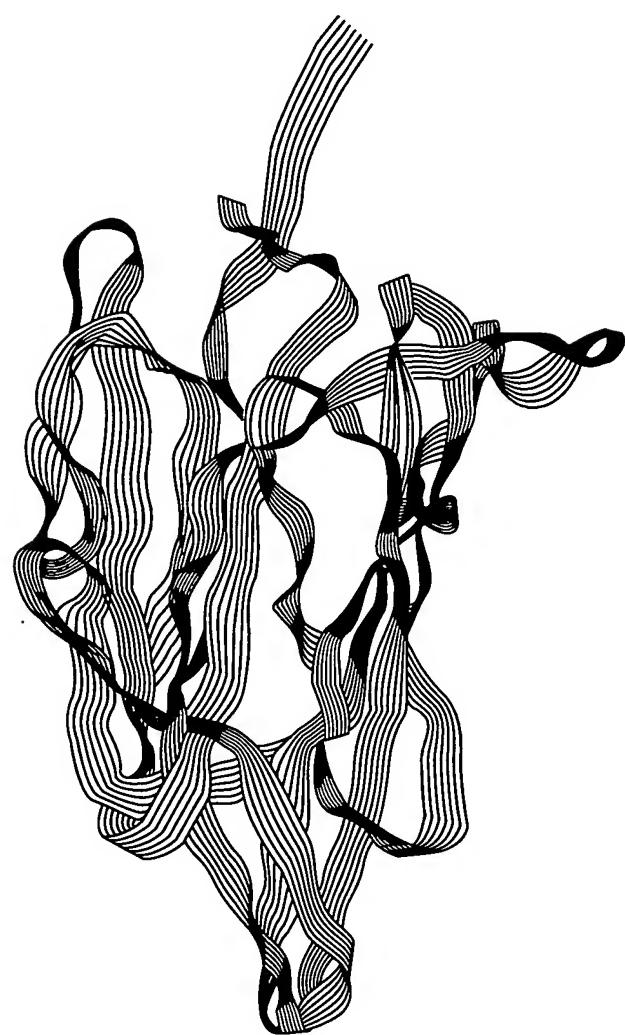


FIG. 5A

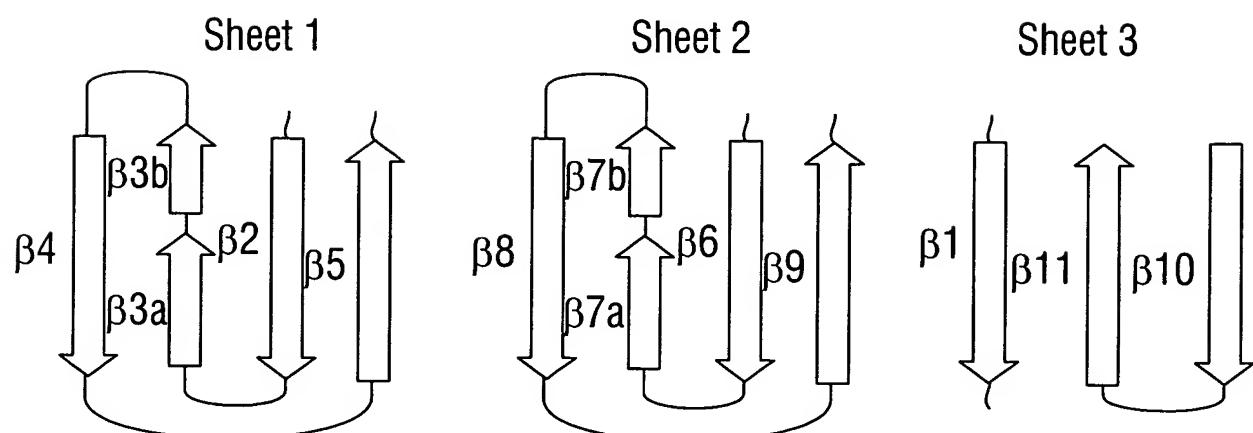


FIG. 5B

Sheet 1

β Strand	Amino Acid Residue
β_2	339-350
β_{3a}	256-360
β_{3b}	362-368
β_4	375-379
β_5	390-395

Sheet 2

β Strand	Amino Acid Residue
β_6	402-412
β_{7a}	416-419
β_{7b}	423-430
β_8	435-442
β_9	452-456

Sheet 3

β Strand	Amino Acid Residue
β_1	296-306
β_{10}	472-483
β_{11}	492-498

FIG. 6

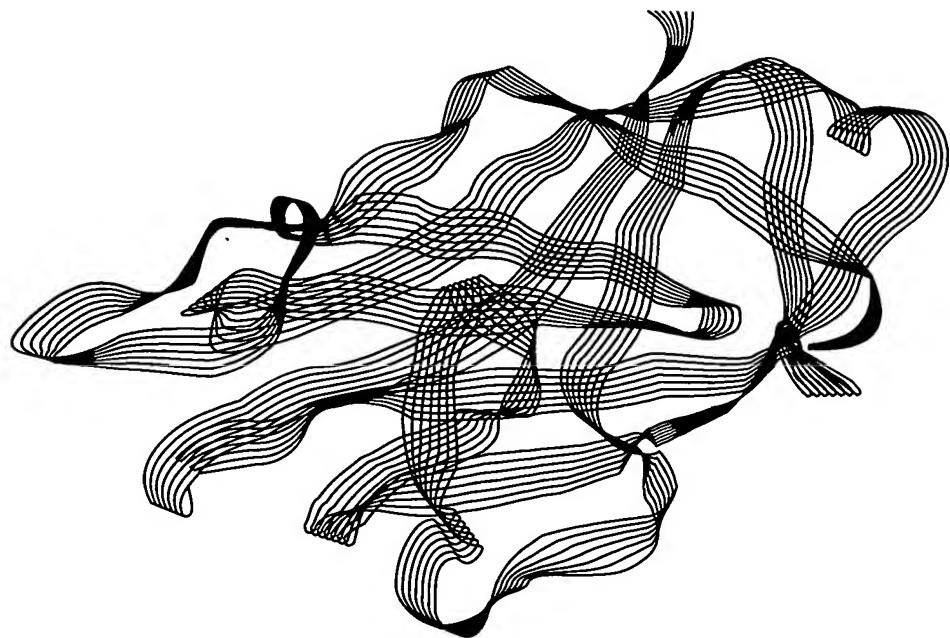


FIG. 7A

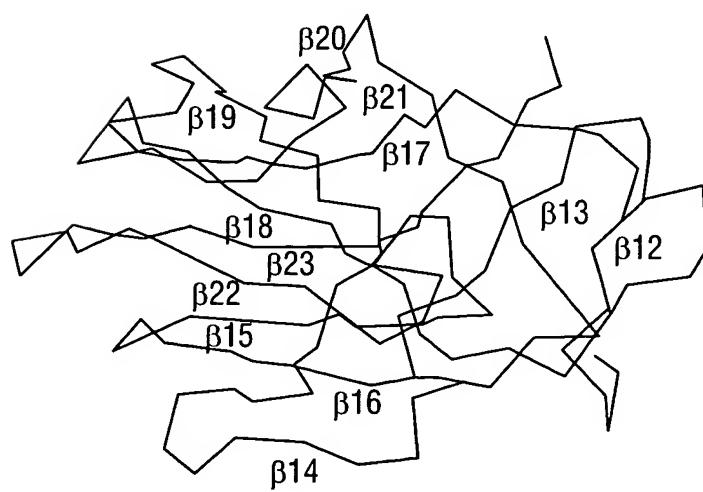


FIG. 7B

Strand Number	Amino Acid Residues
β 12	505-509
β 13	512-515
β 14	522-528
β 15	539-544
β 16	550-557
β 17	563-574
β 18	578-584
β 19	590-596
β 20	609-614
β 21	616-619
β 22	626-636
β 23	638-650

FIG. 8



FIG. 9A

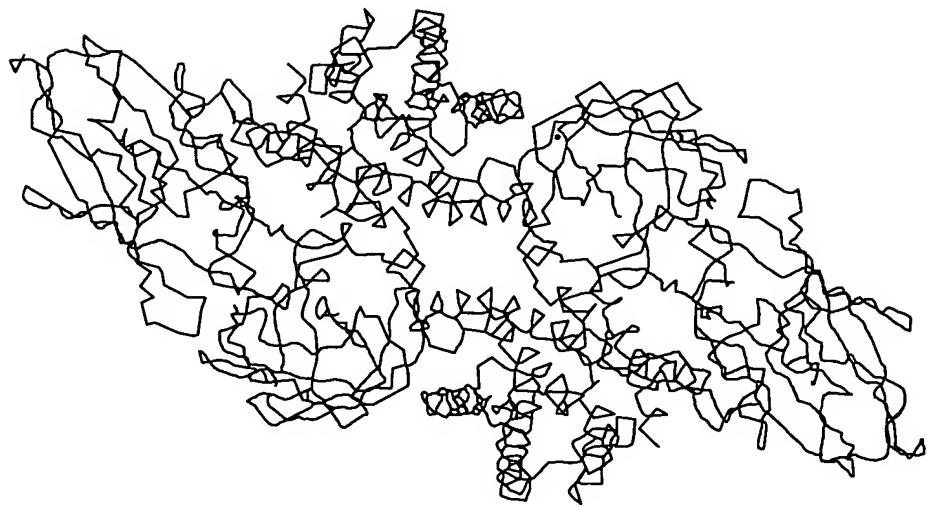


FIG. 9B

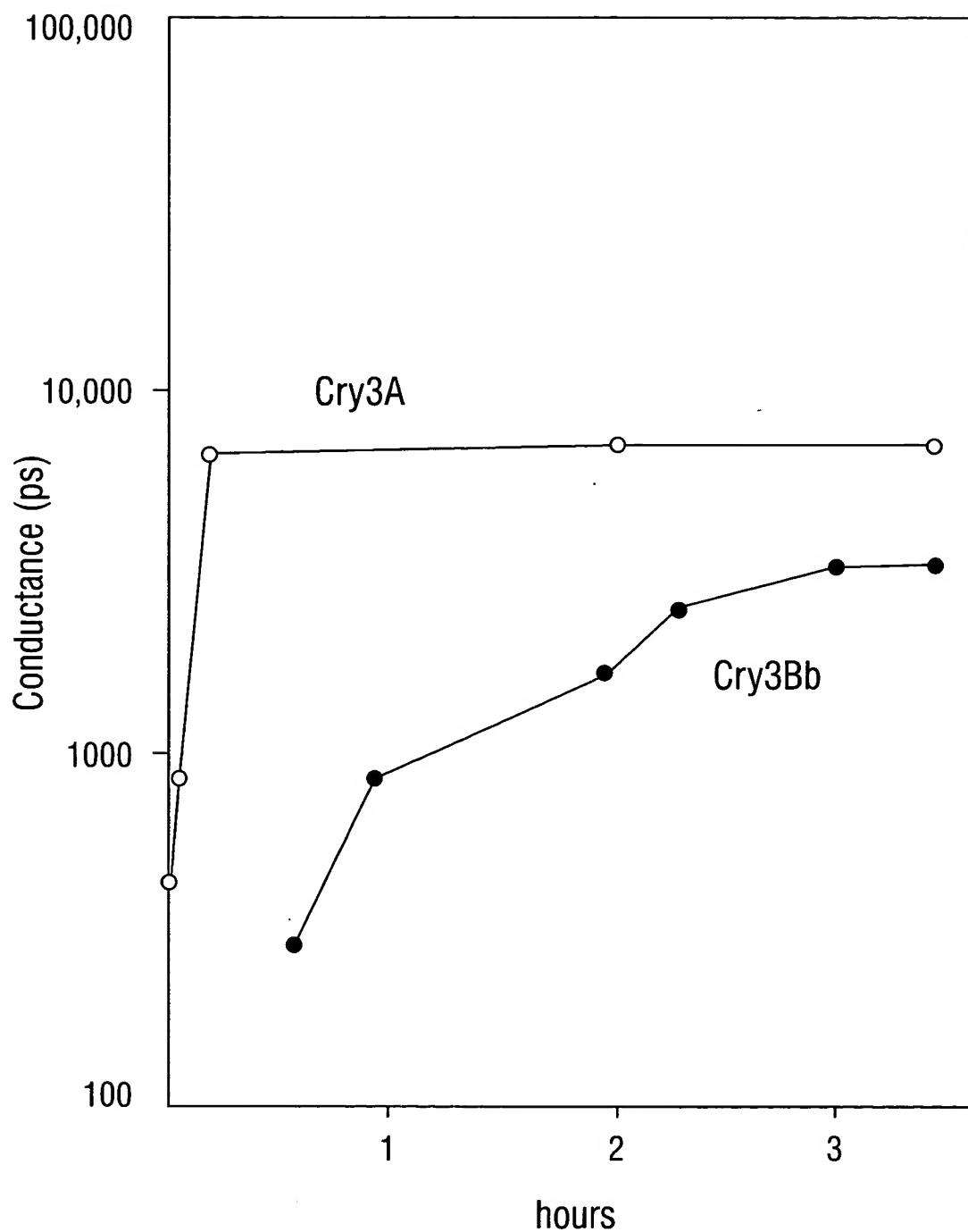


FIG. 10

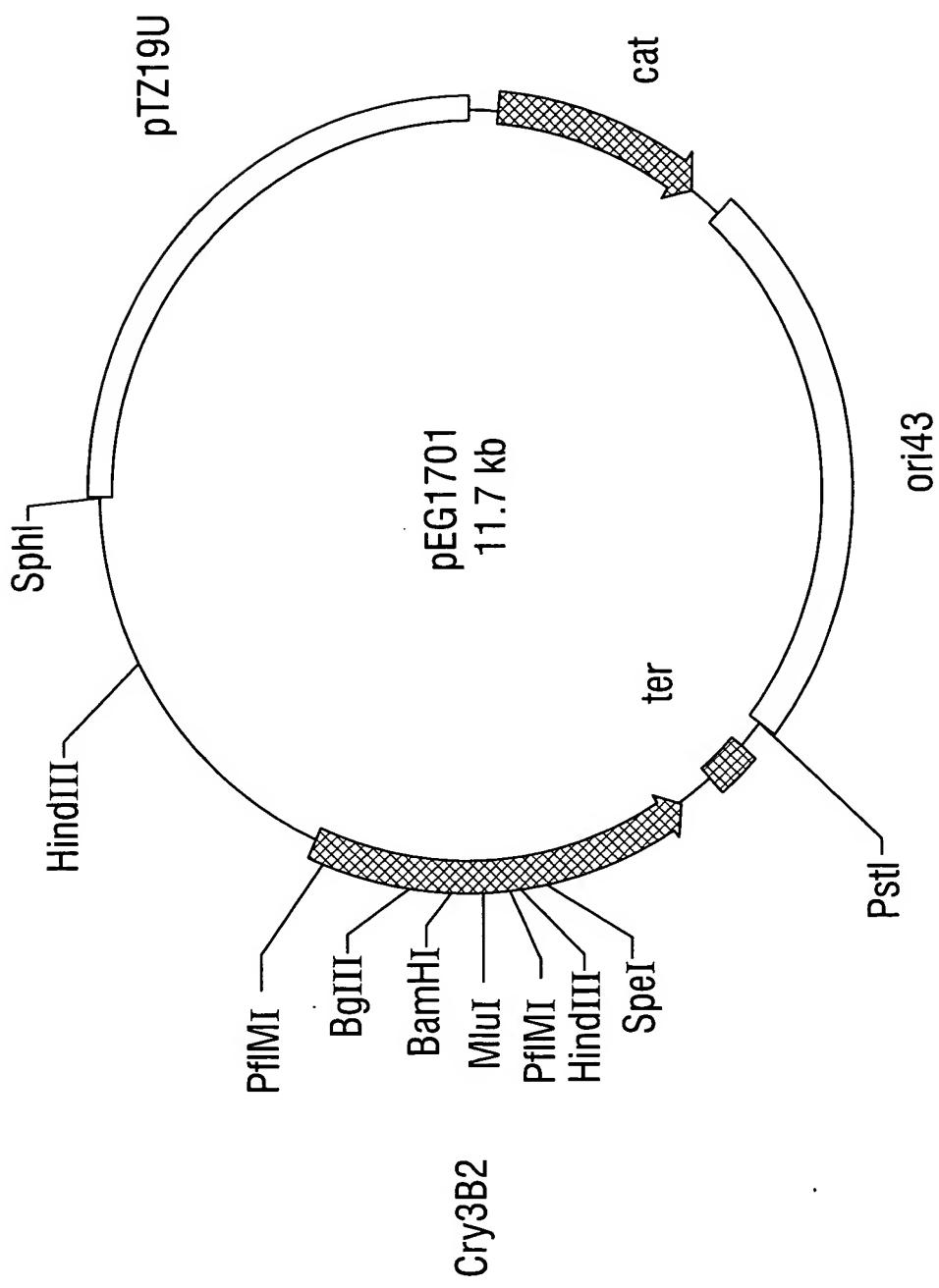


FIG. 11

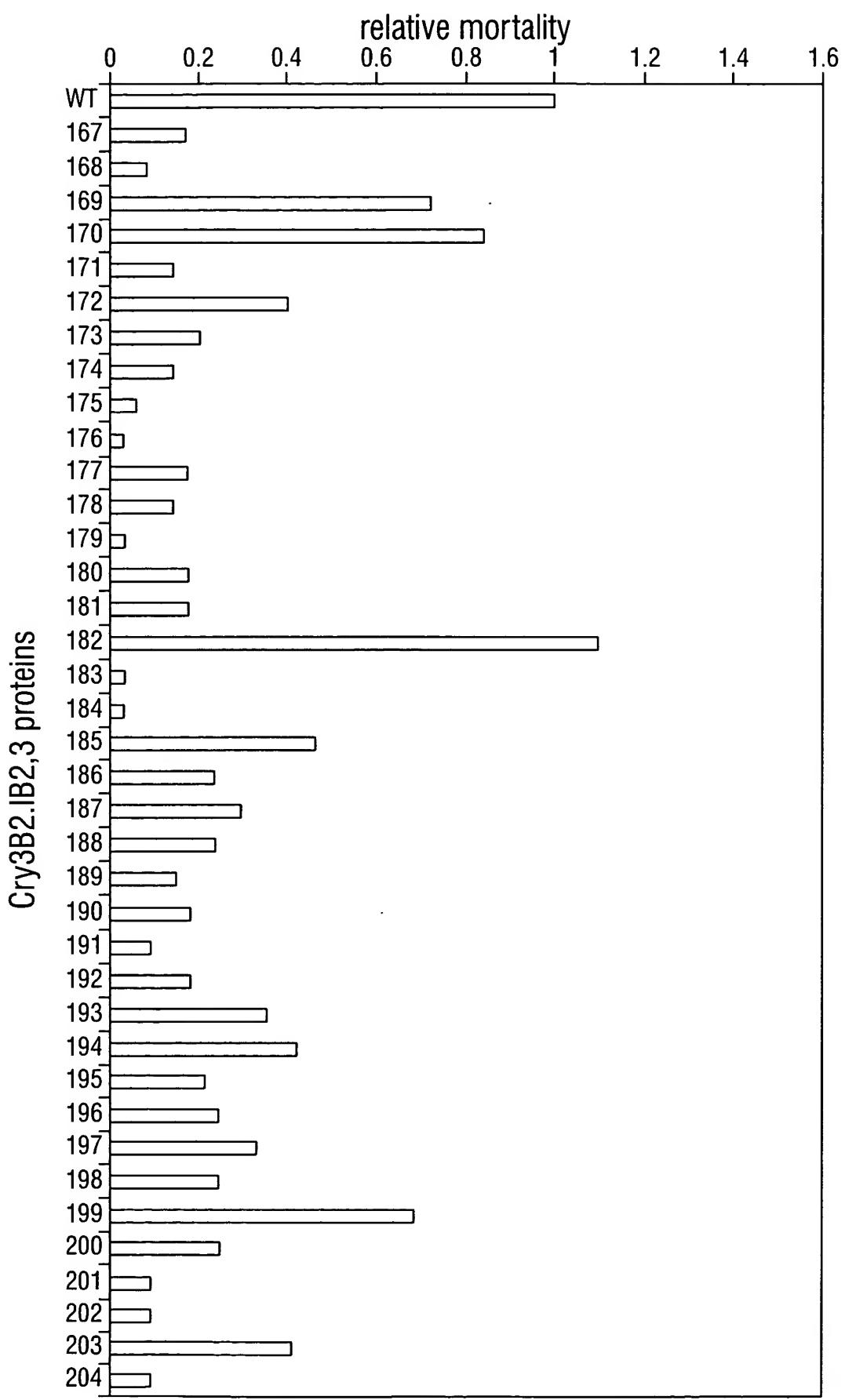


FIG. 12

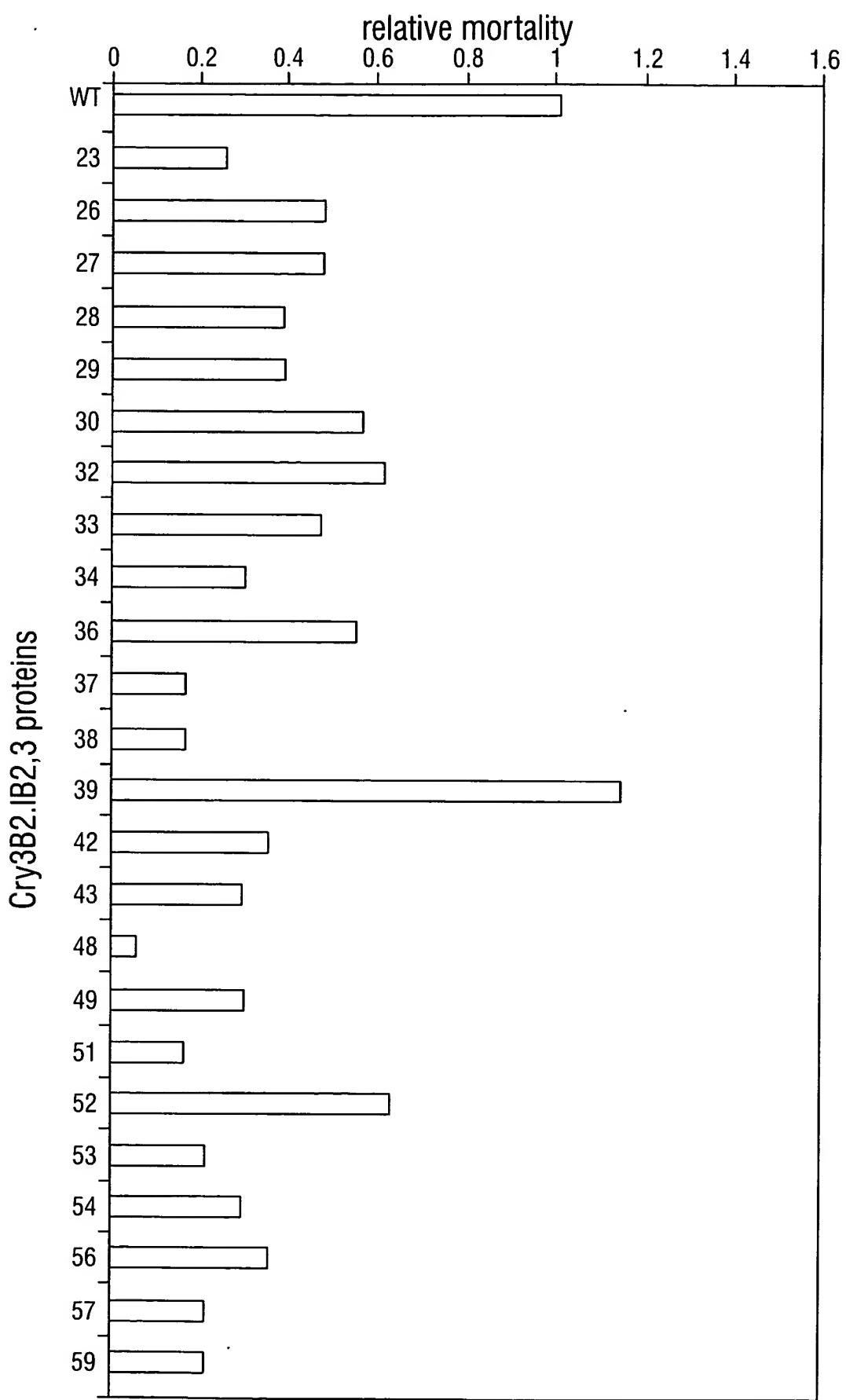


FIG. 13

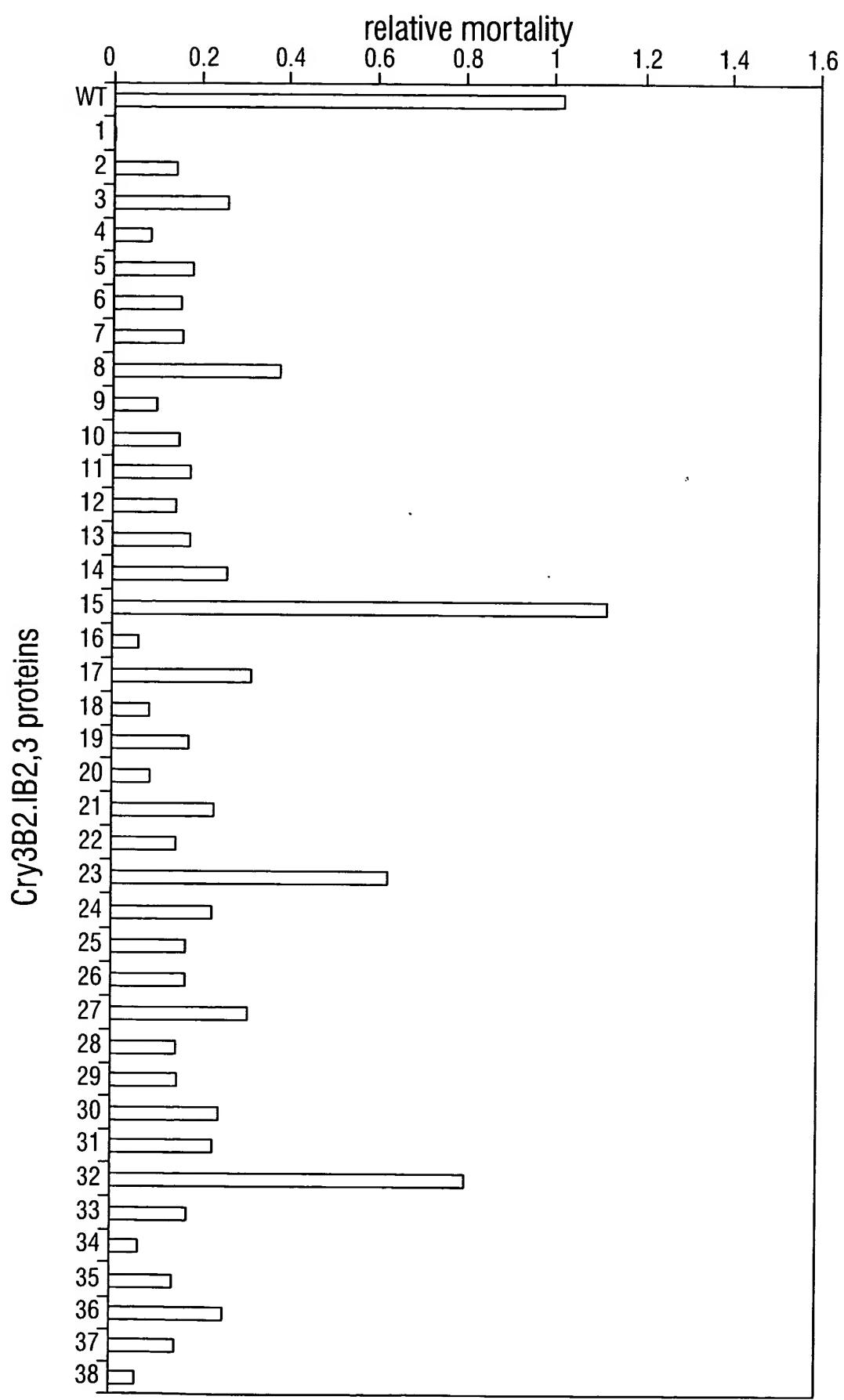


FIG. 14

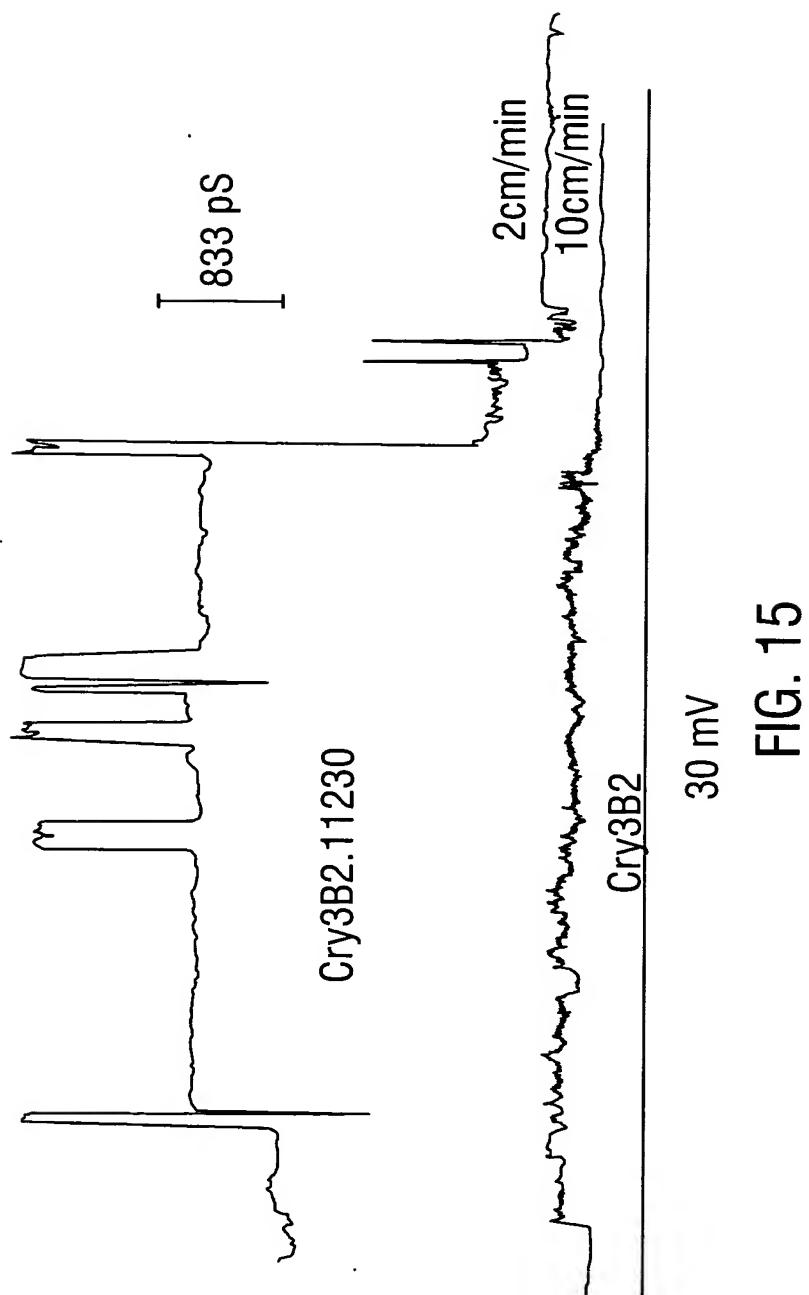


FIG. 15

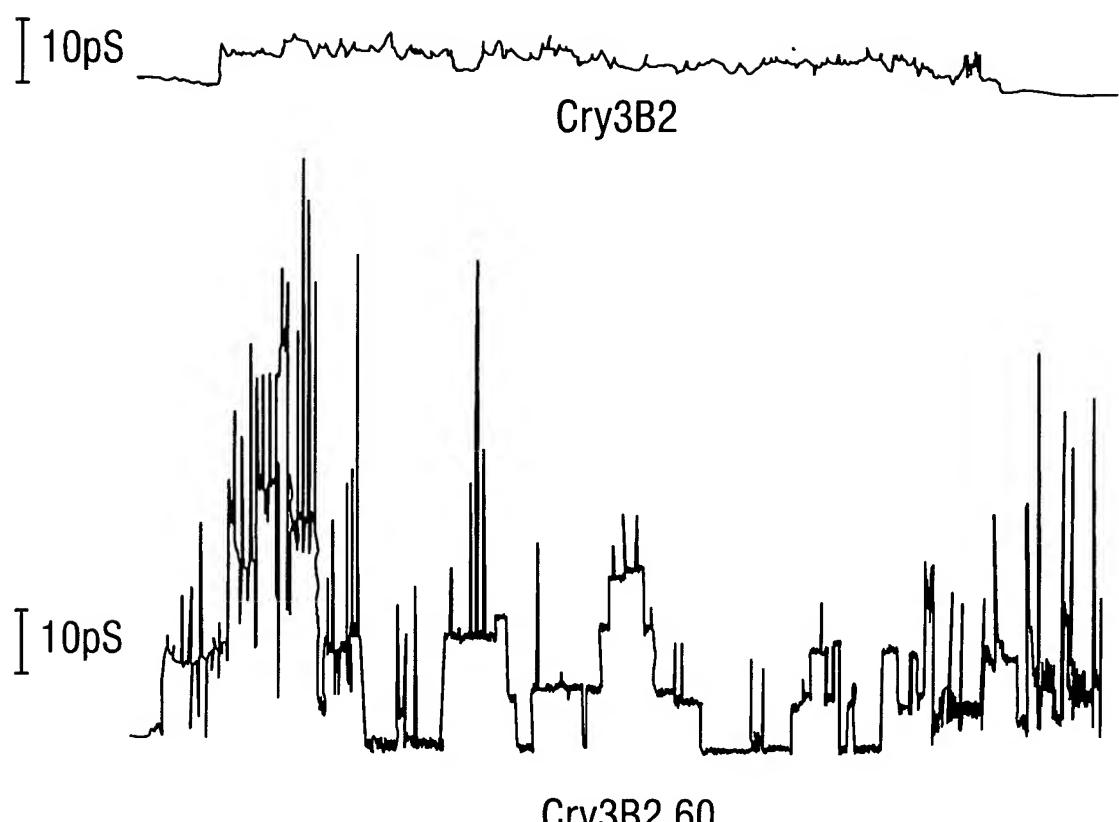


FIG. 16

ALIGNMENT OF CRY3 SEQUENCES
(Numbered according to Cry3BB)
(alpha helices underlined, beta sheets marked with + + +'s)

	1	10	20	30	40
CRY3C:	MNPNNRSEHDTIKATENNEVSNNHAQYPLADTP--TLEELNY				
CRYCBB2:	MNPNNRSEHDTIKVTPNSELPTNHNQYPLADNPNSTLEELNY				
CRY3BB:	MNPNNRSEHDTIKVTPNSELQTNHNQYPLADNPNSTLEELNY				
CRY3BA:	MIRMGGRKMNPNNRSEYDTIKVTPNSELPTNHNQYPLADNPNSTLEELNY				
CRY3A:	MIRKGGRKMNPNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDNY				
	50	60	70	80	90
CRY3C:	KEFLRRRTDNNVEALDSSTTKDAIQKGISIIGDLLGVGVFPYGGALVSFY				
CRYCBB2:	KEFLRMTEDSSTEVLDNSTVKDAVGTGISVVGQILGVGVVPFAGALTSFY				
CRY3BB:	KEFLRMTEDSSTEVLDNSTVKDAVGTGISVVGQILGVGVVPFAGALTSFY				
CRY3BA:	KEFLRMTADNSTEVLDSSSTVKDAVGTGISVVGQILGVGVVPFAGALTSFY				
CRY3A:	KEFLRMTADNNTEALDSSTTK <u>DVIQKGISVVG</u> DLGVGVFPFGGALVSFY				
	100	110	120	130	140
CRY3C:	TNLLNTIWPGE-DPLKAFMQQVEALIDQKIADYAKDKATAELQGLKNVFK				
CRY3BB2:	QSFLDTIWPSSDADPWKAQMVEVLIDKKIEEYAKSKALAEQGLQNNFE				
CRY3BB:	QSFLNTIWPSSDADPWKAQMVEVLIDKKIEEYAKSKALAEQGLQNNFE				
CRY3BA:	QSFLNAIWPSSDADPWKAQMVEVLIDKKIEEYAKSKALAEQGLQNNFE				
CRY3A:	<u>TNFLNTIWPSE-DPWKA</u> FMEQVEALMDQKIADYAKNKALAEQGLQNNVE				
	150	160	170	180	190
CRY3C:	DYVSALDSWDKTPLTLRDGRSQGRIRELFSQAESHFRNSMPSFAVSGYEV				
CRY3BB2:	DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3BB:	DYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3BA:	DYVNALDSWKKAPVNLRSSRSQDRIRELFSQAESHFRNSMPSFAVSKFEV				
CRY3A:	<u>DYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEV</u>				

FIG. 17A

	200	210	220	230	240
CRY3C:	LFLPTYAQAAANTHLLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIEYTN				
CRY3BB2:	LFLPTYAQAAANTHLLLLKDAQVFGEEWGYSSVEDVAEFYHRQLKLTQQYTD				
CRY3BB:	LFLPTYAQAAANTHLLLLKDAQVFGEEWGYSSVEDVAEFYHRQLKLTQQYTD				
CRY3BA:	LFLPTYAQAAANTHLLLLKDAQVFGEEWGYSSEDIAEFYQRQLKLTQQYTD				
CRY3A:	<u>LFLTTYAQAAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTD</u>				
	250	260	270	280	290
CRY3C:	HCAKWKAGLDKLRGSTYEEWVKFNRYRREMTLTVLDLITLFPLYDVRTY				
CRYS3BB2:	HCVNWYNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFYDVRLY				
CRY3BB:	HCVNWYNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFYDIRLY				
CRY3BA:	HCVNWYNVGLNSLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFYDVRLY				
CRY3A:	<u>HCVKWNVGLDKLRGSSYESWVNFnRYRREMTLTVLDLIALFPLYDVRLY</u>				
	300	310	320	330	340
CRY3C:	TKGVKTELTRDVLDPIAVVNNMNGYGTTSFSNIENYIRKPHLFDYLHAIQ				
CRY3BB2:	SKGVKTELTRDIFTDPISLNTLQEYGPFLSIENSIRKPHLFDYLQGIE				
CRY3BB:	SKGVKTELTRDIFTDPISLNTLQEYGPFLSIENSIRKPHLFDYLQGIE				
CRY3BA:	SKGVKTELTRDIFTDPIFTLNALQEYGPFTSSIENSIRKPHLFDYLRGIE				
CRY3A:	PKEVKTELTRDVLDPIVGVNNLRGYGTTSFSNIENYIRKPHLFDYLHRIQ ++++++				
	350	360	370	380	390
CRY3C:	FHSRLQPGYFGTDSFNYWSGNVSTRSSIGSDEIIRSPFYGNKSTLDVQN				
CRY3BB2:	FHTRLQPGYSGKDSFNYWSGNVETRPSIGSSKTITSFYGDKSTEPVQK				
CRY3BB:	FHTRLQPGYFGKDSFNYWSGNVETRPSIGSSKTITSFYGDKSTEPVQK				
CRY3BA:	FHTRLRPGYSGKDSFNYWSGNVETRPSIGSNDTITSFYGDKSIEPIQK				
CRY3A:	FHTRFQPGYYGNDSFNYWSGNVSTRPSIGSNDIITSFYGNKSSEPVQN +++++ +++++ +++++ +++++ +++				
	400	410	420	430	
CRY3C:	LEFNGEKVFRAVANGNLAVWPVGTTGGTKIHSGVTKVQFSQYNDRKDEVRT				
CRY3BB2:	LSFDGQKVYRTIANTDVAAWPNG---KIYFGVTKVDFSQYDDQKNETST				
CRY3BB:	LSFDGQKVYRTIANTDVAAWPNG---KVYLGVTKVDFSQYDDQKNETST				
CRY3BA:	LSFDGQKVYRTIANTDIAFPDG---KIYFGVTKVDFSQYDDQKNETST				
CRY3A:	LEFNGEKVYRAVANTNLAVWPSA---VYSGVTKEFSQYNDQTDEAST +++ +++++++ +++ +++++++ +++				

FIG. 17B

	440	450	460	470	480
CRY3C:	QTYDSKRNVGGIV-FDSIDQLPPIITDESLEKAYSHQLNYVRCFLLQGGR				
CRY3BB2:	QTYDSKRNNNGHVGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BB:	QTYDSKRNNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3BA:	QTYDSKRYNGYLGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR				
CRY3A:	QTYDSKRNVGAVS-WDSIDQLPPETTDEPLEKGYSHQLNYVMCFMLMQGSR				
	+++++	+++++			++++++
	490	500	510	520	530
CRY3C:	GIIPVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNSTSVVAGPGFTGG				
CRY3BB2:	GTIPFFT WTHRSDVFFNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGG				
CRY3BB:	GTIPFFT WTHRSDVFFNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGG				
CRY3BA:	GTIPFFT WTHRSDVFFNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGG				
CRY3A:	GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGG				
	++++++	+++++	+++		++++++
	540	550	560	570	580
CRY3C:	DII-KCT-NGSGLTLYVTAPDLTYSKTYKIRIRYASTSQVRFGIDLGSY				
CRY3BB2:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN				
CRY3BB:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN				
CRY3BA:	NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN				
CRY3A:	DII-QCTENGSAATIYVTPD--VSYSQKYRARIHYASTSQITFTLSLDGA				
	+++++	++++++	+++++ ++++++		++++++
	590	600	610	620	630
CRY3C:	THSISYFDKTMDKGNTLTYNFNLSSVSRPIEISG-GNKIGVSVGGIGSG				
CRY3BB2:	DFIVIYINKTMNIDDDLTQTFDLATTNSNMGFSGDTNELIIGAESFVSN				
CRY3BB:	DFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN				
CRY3BA:	DFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSN				
CRY3A:	PFNQYYFDKTINKGDTLTYNFNLASFSTPFELSG--NNLQIGVTGLSAG				
	++++++	++++++	+++		++++++
	640	650			
CRY3C:	DEVYIDKIEFIPMD				
CRY3BB2:	EKIYIDKIEFIPVQL				
CRY3BB:	EKIYIDKIEFIPVQL				
CRY3BA:	EKIYIDKIEFIPVQ				
CRY3A:	DKVYIDKIEFIPVN				
	++++++				